

GenCore version 6.3  
Copyright (c) 1993 - 2009 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 26, 2009, 03:22:05 ; Search time 27 Seconds  
(without alignments)  
20013.649 Million cell

updates/sec

Title: US-09-300-482-14  
Perfect score: 409  
Sequence: 1  
cccacgcgtccgcggtcatg.....gcaacggcccgctccttgatg 410

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 1681669 seqs, 647077473 residues

Total number of hits satisfying chosen parameters: 3363338

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published\_Applications\_NA\_New:\*  
1:  
/ABSS/Data/CRF/ptodata/2/pubpna/US09\_NEW\_PUB.seq:\*  
2:  
/ABSS/Data/CRF/ptodata/2/pubpna/US10\_NEW\_PUB.seq:\*  
3:  
/ABSS/Data/CRF/ptodata/2/pubpna/US11\_NEW\_PUB.seq:\*  
4:  
/ABSS/Data/CRF/ptodata/2/pubpna/US12\_NEW\_PUB.seq:\*

Pred. No. is the number of results predicted by chance to  
have a  
score greater than or equal to the score of the result being  
printed,  
and is derived by analysis of the total score distribution.